SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Harada, John
        Lotan, Tamar
        Ohto, Masa-aki
        Goldberg, Robert B.
        Fischer, Robert L.
        Bui, Anhthu
        Kwong, Raymond

(ii) TITLE OF INVENTION: Leafy Cotyledon1 Genes and Their Uses

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Townsend and Townsend and Crew LLP
    (B) STREET: Two Embarcadero Center, Eighth Floor
    (C) CITY: San Francisco
    (D) STATE: California
    (E) COUNTRY: USA
    (F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Floppy disk
    (B) COMPUTER: IBM PC compatible
    (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER: US 08/804,534
    (B) FILING DATE: 21-FEB-1997
    (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Bastian, Kevin L.
    (B) REGISTRATION NUMBER: 34,774
    (C) REFERENCE/DOCKET NUMBER: 023070-077600US

(ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: (415) 576-0200
    (B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..627
(D) OTHER INFORMATION: /product= "LEC1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG ACC AGC TCA GTC ATA GTA GCC GGC GCC GGT GAC AAG AAC AAT GGT
48
Met Thr Ser Ser Val Ile Val Ala Gly Ala Gly Asp Lys Asn Asn Gly
 1   5   10   15

ATC GTG GTC CAG CAG CAA CCA CCA TGT GTG GCT CGT GAG CAA GAC CAA
96
Ile Val Val Gln Gln Gln Pro Pro Cys Val Ala Arg Glu Gln Asp Gln
             20   25   30

TAC ATG CCA ATC GCA AAC GTC ATA AGA ATC ATG CGT AAA ACC TTA CCG
144
Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Thr Leu Pro
             35   40   45

TCT CAC GCC AAA ATC TCT GAC GAC GCC AAA GAA ACG ATT CAA GAA TGT
192
Ser His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys
       50   55   60

GTC TCC GAG TAC ATC AGC TTC GTG ACC GGT GAA GCC AAC GAG CGT TGC
240
Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys
 65   70   75   80

CAA CGT GAG CAA CGT AAG ACC ATA ACT GCT GAA GAT ATC CTT TGG GCT
288
Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Ile Leu Trp Ala
             85   90   95

ATG AGC AAG CTT GGG TTC GAT AAC TAC GTG GAC CCC CTC ACC GTG TTC
336
Met Ser Lys Leu Gly Phe Asp Asn Tyr Val Asp Pro Leu Thr Val Phe
         100   105   110

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ATT AAC CGG TAC CGT GAG ATA GAG ACC GAT CGT GGT TCT GCA CTT AGA
384
Ile Asn Arg Tyr Arg Glu Ile Glu Thr Asp Arg Gly Ser Ala Leu Arg
        115           120           125

GGT GAG CCA CCG TCG TTG AGA CAA ACC TAT GGA GGA AAT GGT ATT GGG
432
Gly Glu Pro Pro Ser Leu Arg Gln Thr Tyr Gly Gly Asn Gly Ile Gly
    130           135           140

TTT CAC GGC CCA TCT CAT GGC CTA CCT CCT CCG GGT CCT TAT GGT TAT
480
Phe His Gly Pro Ser His Gly Leu Pro Pro Pro Gly Pro Tyr Gly Tyr
145           150           155           160

GGT ATG TTG GAC CAA TCC ATG GTT ATG GGA GGT GGT CGG TAC TAC CAA
528
Gly Met Leu Asp Gln Ser Met Val Met Gly Gly Gly Arg Tyr Tyr Gln
        165           170           175

AAC GGG TCG TCG GGT CAA GAT GAA TCC AGT GTT GGT GGT GGC TCT TCG
576
Asn Gly Ser Ser Gly Gln Asp Glu Ser Ser Val Gly Gly Gly Ser Ser
    180           185           190

TCT TCC ATT AAC GGA ATG CCG GCT TTT GAC CAT TAT GGT CAG TAT AAG
624
Ser Ser Ile Asn Gly Met Pro Ala Phe Asp His Tyr Gly Gln Tyr Lys
    195           200           205

                                        627
TGA
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 208 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Thr Ser Ser Val Ile Val Ala Gly Ala Gly Asp Lys Asn Asn Gly
1         5           10          15

Ile Val Val Gln Gln Gln Pro Pro Cys Val Ala Arg Glu Gln Asp Gln
        20          25          30
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Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Thr Leu Pro
    35   40   45

Ser His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys
    50   55   60

Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys
    65   70   75   80

Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Ile Leu Trp Ala
        85   90   95

Met Ser Lys Leu Gly Phe Asp Asn Tyr Val Asp Pro Leu Thr Val Phe
     100   105   110

Ile Asn Arg Tyr Arg Glu Ile Glu Thr Asp Arg Gly Ser Ala Leu Arg
     115   120   125

Gly Glu Pro Pro Ser Leu Arg Gln Thr Tyr Gly Gly Asn Gly Ile Gly
     130   135   140

Phe His Gly Pro Ser His Gly Leu Pro Pro Pro Gly Pro Tyr Gly Tyr
 145   150   155   160

Gly Met Leu Asp Gln Ser Met Val Met Gly Gly Gly Arg Tyr Tyr Gln
     165   170   175

Asn Gly Ser Ser Gly Gln Asp Glu Ser Ser Val Gly Gly Gly Ser Ser
     180   185   190

Ser Ser Ile Asn Gly Met Pro Ala Phe Asp His Tyr Gly Gln Tyr Lys
     195   200   205

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3395 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGATCCAAAA CAGGTCATGG ACTGGGCCGT AAACTCTATC CAAAATTCTT CATGTTTTTC   60

CATCTTTCAA AAATCTTTAT CCACCATTCC ATTACTAGGG TGTTGGTTTT ATTTTATTTG   120

TTGATTAATT ATGTATTAGA AAATGTAAAG CAATATTCAA TTGTAACATG CATCATCTAA   180

CACCAATATC TTGTACTAAC CTTTTGTAAT TTTCCTATAA ACATTTTAAA AGGCTAATTT 240

AAATAAAAAT TACAATAAAC GTGATAACTC ACTTTCGTAA CGCATATTTA TTCAAATATA 300

CCAAAATTTA CCATTTTAAG TAAGAGAATC TTTTTAAAAT TAATTTTCAA TTTCATTAAT 360

TAAGAAACAA AGAATTTACT GAAACCTATA TTTTATTAAA TTTTAATAAA ATATATGACT 420

AAAATAACGT CACGTGAATC TTTCTCAGCC GTTCGATAAT CGAATACTTT ATTGACTAAG 480

TATTTATTTA GAAAATTTTA AACAACACTT AATTTCTAGA AACAAAGAGA GCCTCATATG 540

TATAAAAATC TTCTTCTTAT CTTTCTTTCT TTCTTAATAG TCTTTATTTT TACTTAATTA 600

CTTTGGTAAT TTGTGAAAAA CACAACCAAT GAGAGAAGAG CAGTTTGACT GGCCACATAG 660

CCAATGAGAC AAGCCAATGG GAAAGAGATA TAGAGACCTC GTAAGAACCG CTCCTTTGCC 720

ATTTGTATCA TCTCTCTATA AAACCACTCA ACCATCAACC TNTCTTTGCA TGCAACAAAT 780

CACTCAAATA ATTATTTTAT AAAGAACAAA AAAAAAAGA CGGCAGAGAA ACAATGGAAC 840

GTGGAGCTCC CTTCTCTCAC TATCAGCTAC CCAAATCCAT CTCTGGTAAT CTAAGTGGCT 900

ATTTGTATAC AGTATATACT TGCCTCCATG TATATTTATA TTCTCGTGAA AAATTGGAGA 960

CATGCTTTAT GAATTTTATG AGACTTTGCA ACAACGAACG AGATGCTTTC TCTCTAGAAA 1020

TTTAAATTTA GATTTGTGAA GGTTTTGGGA ATGGCCCGGA GAAGACGATT TTATATATAC 1080

ATGCATGCAA GAGTTTGATA TGTATATTGT TTCATCATGG CTGAGTCAAA GTTTTATCCA 1140

AATATTTCCA TGGTGTGGTA TTAGTTAAAC AAATCTCTCG TATGTGTCAT TGAATATACC 1200

CGTGCATGTA CCAGGAATGT TTTTGATTCT AAAAACGTTT TTTTCTTTGT TGTAACGGTT 1260

GAGTTTTTTT CTTCGTTTCA AAACGAGATT CTCGTTTGTC TCTTCCCTTG TCTAAAAACA 1320

TCTACGGTTC ATGTGATTCA AAAACACTAA AAAAATATAA ACTCATTTTT TTTTAATACT 1380

TAACATTTAA ACTATATATA TATATATATA TATATATATC TTATACTAGT CCCAAGTTTT 1440

AGTGTGAGGT TTTTTTATTC AAAATCTATC AGTACATTTT TTGGAAAAGA ACTAAGTGAA 1500

ATTTTCTCCA AATTTTCCTT TTACTATTGA TTTTTTAATT ACTGGATGTC ATTAACTTTA 1560

ATCTTTTGAT TCTTTCAACG TTTACCATTG GGAACCTTCA CATGAAATAA ATGTCTACTT 1620

TATTGAGTCA TACCTTCGTC AACATAAATT AATTGATGTT CTTCTCCAAA TTTTGAGTTT 1680

TTGGTTTTTC TAATAATCTT AACGAAAGCT TTTTGGTATA CATGTAAAAC GTAACGGCAA 1740

GAATCTGAAC AGTCTACTCA ACGGGGTCCA TAAGTCTAGA ATGTAGACCC CACAAACTTA 1800

CTCTTATCTT ATTGGTCCGT AACTAAGAAC GTGTCCCTCT GATTCTCTTG TTTTCTTCTA 1860

ATTAATTCGT ATCCTACAAA TTTAATTATC ATTTCTACTT CAACTAATCT TTTTTTATTT 1920

CCTAAAGATT TCAATTTCTC TCTGTATTTT CTATGAACAG AATTGAACTT GGACCAGCAC 1980

AGCAACAACC CAACCCCAAT GACCAGCTCA GTCATAGTAG CCGGCGCCGG TGACAAGAAC 2040

AATGGTATCG TGGTCCAGCA GCAACCACCA TGTGTGGCTC GTGAGCAAGA CCAATACATG 2100

CCAATCGCAA ACGTCATAAG AATCATGCGT AAAACCTTAC CGTCTCACGC CAAAATCTCT 2160

GACGACGCCA AAGAAACGAT TCAAGAATGT GTCTCCGAGT ACATCAGCTT CGTGACCGGT 2220

GAAGCCAACG AGCGTTGCCA ACGTGAGCAA CGTAAGACCA TAACTGCTGA AGATATCCTT 2280

TGGGCTATGA GCAAGCTTGG GTTCGATAAC TACGTGGACC CCCTCACCGT GTTCATTAAC 2340

CGGTACCGTG AGATAGAGAC CGATCGTGGT TCTGCACTTA GAGGTGAGCC ACCGTCGTTG 2400

AGACAAACCT ATGGAGGAAA TGGTATTGGG TTTCACGGCC CATCTCATGG CCTACCTCCT 2460

CCGGGTCCTT ATGGTTATGG TATGTTGGAC CAATCCATGG TTATGGGAGG TGGTCGGTAC 2520

TACCAAAACG GGTCGTCGGG TCAAGATGAA TCCAGTGTTG GTGGTGGCTC TTCGTCTTCC 2580

ATTAACGGAA TGCCGGCTTT TGACCATTAT GGTCAGTATA AGTGAAGAAG GAGTTATTCT 2640

TCATTTTTAT ATCTATTCAA AACATGTGTT TCGATAGATA TTTTATTTTT ATGTCTTATC 2700

AATAACATTT CTATATAATG TTGCTTCTTT AAGGAAAAGT GTTGTATGTC AATACTTTAT 2760

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CCAAGCCAAA AGGTTATAAA ATCTAAATTC GTTGAGTTGT CAAACTTCTG AAGATTGCTA 3000

TCCTCTTTGA GTTGCTTTCT TTTGGGTGCT TGAGTTTCAT TAGGCTGAGC TGACTCGTTG 3060

CTCTCTAGTC TTTCATCTCT GTCTTTTCCA AGGATTCATA ACGTTGGTCG CTCTCTGTTT 3120

CTGCCTACAC TTCTTCAAGG GATCATTACT GAGGCTAAGA GTTAAAGACC TGAACCATGG 3180

TTTTCTGTAA CTGGTTCAAG TTCATTCTCC GGTTATTGTG TGGTTATCTT TCGGTTAGAT 3240

TGAAACCCAT ATGTTTGCTC TGTTTCTTCT AGTTCCAAGT TTAATTTCCG GTTATTGTTT 3300

GGCTTTTTAA AAGTTTTTAA GGTCTATTCT ATGTAAAGAC TATTCTACGT ACGTACATTT 3360

ATCGCAAAAT TGAAAGATTA TAAAAAAAAT TGAAA   3395

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7560 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTNACCCT CACTAAAGGG AACAAAAGCT GGGTACCGGG CCCCCCCTCG
AGGTCGACGG   60

TATCGATAAG CTTGATATCG AATTCGTGGC CATTAGACCC ATAACTATAT
GACGATGTTA   120

AAGAGAAAAT AAATCATAAA TAAAATAAGA GTCCTTATCA ATAAACCTAA
TTGGCTAATT   180

TCAACCTCAA AGAGTAGTAG GAACAGGTAA GGTGAAGCCA AACAGCTCCT
TTTACAGTTG   240

GACCACTAGA GCTGATCTGG CATACAAAGT ATGCTTATTG GGCTGTCACG
GCCCATCCGC   300

AAAATGTCGT TGGTTACGAA GCATCCACGA CATAGACGGT GCCACATGTT
AGAAAAGTGT   360

TTCGGCGATC AAGATTGTGT CCACATCATT AGACGTCTGA ACTGTCCACG
TGTCTATCAA   420

AGCTGGCGTC AAACATTACG TTTTCGTCGT TTGCGCCTCC TAGTTCACAC
GTGCAACGAA   480

CGCGTGCGAC GTATCAAAAT TGTTAATTTT AGCCATGTAT AAAGAATATC
TACAAAATTA   540

ACCTCAGGAA TATTTTTGTT TTTTCAATTG AGGCCATAAT ATACNTNCCG
ATNGAAAAAT   600

TTTNCANCAT ATCNCTAATA TCAAAAAATT ATGATGTTAG TAAACGTAAA
AAATTTACAC   660

AAAATAANTT TCACAAAACT TANNGGGGAA ATTGGAACAA ANAAAAGACT
GGTGAGTGAT   720

AAGCGATGAT GGCCGGTGAA TCAGGTAGCC GTCCTACAAC GTGGTTGATT
TTGAGCAAAC   780

TCCTATCTAC TCTTCACACT ATTGGAAATC CCAAAATGTC GTCACACCAT
AATAATGTGA   840

ATTTTGTTAT GGAATTTGAG GGAAACAGTA GATATATGTT TCAACCAGTG
AAAGTTACCC   900

TCCTTTGGAC ATATCTACGA NAGTAGAAAG TAGAAACATT CACTAAACGT
GACAACTTTA   960

TAAATTTTCT TTTTGTAACT TTTCTTTAGA TTTATTTACG ANAAGAGAAA
TATAAACGTC   1020

ATGCTAATAA AAAATGCATT ATTTTCTACC ATCTAGCTAG AATATTGATC
AAGTCTTCAC   1080

GTTTTTTGTT TATCTCTTCT CTCATAGGCA TGTCCACAAA AGGGTAAGTT
TTACTGGTTC   1140

AAAATATTGC ATGAGTACTA CTAAGCTCGT ATAGTTTGAT CTTACTATCA
TTGCGATGAG   1200

GGTTGTTAGT TTGGAAGAAA TAAGGATTTA TGCAAATGGT AATCATTATG
TCTGCTATTT   1260

AAGAAGTAAA TTATGATGCT TGTTGCGTGA ACATATTAAA TTTGCGAAAA
ATAAGCAAGG   1320

ATACACGAGA GAAGCTCAGA TATTCACGTA ACGATGTTTC ATCTCTTCTC
ATTGAGGAAA   1380

CATATGGCCA TGATATAGCT AATAAGCCTA CGGGATTGTC NTTTCAACGC
CGAATCTACC   1440

AAACTGTTCC ATCTCTTATT ATATATAGTT TGGTTATTTA AGTAATTAGA
TGCATCATAA   1500

TCTTTTTTTC TGCCAGTTGT AATGCAGATA AAAATATATT GGTTGTTCTA
AGGATTGTTC   1560

AAACGTGCAT GTGTACAAGT TATTATTTAT ATACTTTCAT CTACATGCGA
TGCGTTATTT   1620

ATAATGATAA AACTAAGATT TTTAGTTAAA TTTAATAAAG AGCTTACGAG
CTACAATTAA   1680

TTAGAAATGG TTGCTCAGAA ATCAGAATAC TATATATGAA AAAAGAAGTT
GGTATACTTG   1740

AAAAAAGAAA AAACTACTTG AAAAGATGGT AAAAGATATA GAACGAGTAT
ATATCTTACT   1800

CAAGCACGAT AGAAGTTTGT ATCAAAACAT TGCGTTCCAA ACCAATGTTT
GAAGATGGTC   1860

AAAGGTGCTA CTCATGATGT GGTGCGAAGA AGCTTACGAA AAATTCTGCA
ATGAGAGATA   1920

ACTTTATGGG CTGCTTGTTC AATATATTGA AAATCATGGT AGACAACACC
AAACTCTCCT   1980

TTACCAGAAG TCATATTTCC TTAACCTCAG AATAAGTAAA TCTTCTAGTT
TATTATTTGA   2040

AAGTTGAGCG TATAATTGCA ATGAAACTTT TACCAATTCA CCGCCTCCTA
ACTGAGTTGT   2100

TGTATTATCC TATCTCTTTA GCTATCCTTT CCTTGCTCTT GCTCCACCTG
CATGTGGCCT   2160

CTTTATTTAT AATCTCTCTA GATTCTGCTA AAGATGTNTG TTCAAAATGG
TTTATCTTTA   2220

AGGGAAGCAA AGTGAATGGA AACATTTAAA GAAAAAAAAA ACTTTTAGCA
GAGTTCCATG   2280

AGATTTCATA CTGATGATAA CTAAAATAAT CTTATATGCG TAAGATTATT
TTAGTTCTAA   2340

ACTTCATTTT GAAATGAGAG GTCATTGGCC AGGAAAGATT CAATATTGGT
TCTTTGTTAA   2400

TTCTCGTTGG TTTGTTTTTA GTATGGGCTA GATCCAAAAC AGGTCATGGA
CTGGGCCGTA   2460

AACTCTATCC AAAATTCTTC ATGTTTTTCC ATCTTTCAAA AATCTTTATC
CACCATTCCA   2520

TTACTAGGGT GTTGGTTTTA TTTTATTTGT TGATTAATTA TGTATTAGAA
AATGTAAAGC   2580

AATATTCAAT TGTAACATGC ATCATCTAAC ACCAATATCT TGTACTAACC
TTTTGTAATT   2640

TTCCTATAAA CATTTTAAAA GGCTAATTTA AATAAAAATT ACAATAAACG
TGATAACTCA   2700

CTTTCGTAAC GCATATTTAT TCAAATATAC CAAAATTTAC CATTTTAAGT
AAGAGAATCT   2760

TTTTAAAATT AATTTTCAAT TTCATTAATT AAGAAACAAA GAATTTACTG
AAACCTATAT   2820

TTTATTAAAT TTTAATAAAA TATATGACTA AAATAACGTC ACGTGAATCT
TTCTCAGCCG   2880

TTCGATAATC GAATACTTTA TTGACTAAGT ATTTATTTAG AAAATTTTAA
ACAACACTTA   2940

ATTTCTAGAA ACAAAGAGAG CCTCATATGT ATAAAAATCT TCTTCTTATC
TTTCTTTCTT   3000

TCTTAATAGT CTTTATTTTT ACTTAATTAC TTTGGTAATT TGTGAAAAAC
ACAACCAATG   3060

AGAGAAGAGC AGTTTGACTG GCCACATAGC CAATGAGACA AGCCAATGGG
AAAGAGATAT   3120

AGAGACCTCG TAAGAACCGC TCCTTTGCCA TTTGTATCAT CTCTCTATAA
AACCACTCAA   3180

CCATCAACCT NTCTTTGCAT GCAACAAATC ACTCAAATAA TTATTTTATA
AAGAACAAAA   3240

AAAAAAAGAC GGCAGAGAAA CAATGGAACG TGGAGCTCCC TTCTCTCACT
ATCAGCTACC   3300

CAAATCCATC TCTGGTAATC TAAGTGGCTA TTTGTATACA GTATATACTT
GCCTCCATGT   3360

ATATTTATAT TCTCGTGAAA AATTGGAGAC ATGCTTTATG AATTTTATGA
GACTTTGCAA   3420

CAACGAACGA GATGCTTTCT CTCTAGAAAT TTAAATTTAG ATTTGTGAAG
GTTTTGGGAA   3480

TGGCCCGGAG AAGACGATTT TATATATACA TGCATGCAAG AGTTTGATAT
GTATATTGTT   3540

TCATCATGGC TGAGTCAAAG TTTTATCCAA ATATTTCCAT GGTGTGGTAT
TAGTTAAACA   3600

AATCTCTCGT ATGTGTCATT GAATATACCC GTGCATGTAC CAGGAATGTT
TTTGATTCTA   3660

AAAACGTTTT TTTCTTTGTT GTAACGGTTG AGTTTTTTTC TTCGTTTCAA
AACGAGATTC   3720

TCGTTTGTCT CTTCCCTTGT CTAAAAACAT CTACGGTTCA TGTGATTCAA
AAACACTAAA   3780

AAAATATAAA CTCATTTTTT TTTAATACTT AACATTTAAA CTATATATAT
ATATATATAT   3840

ATATATATCT TATACTAGTC CCAAGTTTTA GTGTGAGGTT TTTTTATTCA
AAATCTATCA   3900

GTACATTTTT TGGAAAAGAA CTAAGTGAAA TTTTCTCCAA ATTTTCCTTT
TACTATTGAT   3960

TTTTTAATTA CTGGATGTCA TTAACTTTAA TCTTTTGATT CTTTCAACGT
TTACCATTGG   4020

GAACCTTCAC ATGAAATAAA TGTCTACTTT ATTGAGTCAT ACCTTCGTCA
ACATAAATTA   4080

ATTGATGTTC TTCTCCAAAT TTTGAGTTTT TGGTTTTTCT AATAATCTTA
ACGAAAGCTT   4140

TTTGGTATAC ATGTAAAACG TAACGGCAAG AATCTGAACA GTCTACTCAA
CGGGGTCCAT   4200

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ACTAAGAACG   4260

TGTCCCTCTG ATTCTCTTGT TTTCTTCTAA TTAATTCGTA TCCTACAAAT
TTAATTATCA   4320

TTTCTACTTC AACTAATCTT TTTTTATTTC CTAAAGATTT CAATTTCTCT
CTGTATTTTC   4380

TATGAACAGA ATTGAACTTG GACCAGCACA GCAACAACCC AACCCCAATG
ACCAGCTCAG   4440

TCATAGTAGC CGGCGCCGGT GACAAGAACA ATGGTATCGT GGTCCAGCAG
CAACCACCAT   4500

GTGTGGCTCG TGAGCAAGAC CAATACATGC CAATCGCAAA CGTCATAAGA
ATCATGCGTA   4560

AAACCTTACC GTCTCACGCC AAAATCTCTG ACGACGCCAA AGAAACGATT
CAAGAATGTG   4620

TCTCCGAGTA CATCAGCTTC GTGACCGGTG AAGCCAACGA GCGTTGCCAA
CGTGAGCAAC   4680

GTAAGACCAT AACTGCTGAA GATATCCTTT GGGCTATGAG CAAGCTTGGG
TTCGATAACT   4740

ACGTGGACCC CCTCACCGTG TTCATTAACC GGTACCGTGA GATAGAGACC
GATCGTGGTT   4800

CTGCACTTAG AGGTGAGCCA CCGTCGTTGA GACAAACCTA TGGAGGAAAT
GGTATTGGGT   4860

TTCACGGCCC ATCTCATGGC CTACCTCCTC CGGGTCCTTA TGGTTATGGT
ATGTTGGACC   4920

AATCCATGGT TATGGGAGGT GGTCGGTACT ACCAAAACGG GTCGTCGGGT
CAAGATGAAT   4980

CCAGTGTTGG TGGTGGCTCT TCGTCTTCCA TTAACGGAAT GCCGGCTTTT
GACCATTATG   5040

GTCAGTATAA GTGAAGAAGG AGTTATTCTT CATTTTTATA TCTATTCAAA
ACATGTGTTT   5100

CGATAGATAT TTTATTTTTA TGTCTTATCA ATAACATTTC TATATAATGT
TGCTTCTTTA   5160

AGGAAAAGTG TTGTATGTCA ATACTTTATG AGAAACTGAT TTATATATGC
AAATGATTGA   5220

ATCCAAACTG TTTTGTGGAT TAAACTCTAT GCAACATTAT ATATTTACAT
GATCTAAAGG   5280

TTTTGTAATT CAAAAGCTGT CATAGTTAGA AGATAACTAA ACATTGTAGT
AACCAAGTTT   5340

AATTTACTTT TTTGAGTTTA CATAACTAAC CAAGCCAAAA GGTTATAAAA
TCTAAATTCG   5400

TTGAGTTGTC AAACTTCTGA AGATTGCTAT CCTCTTTGAG TTGCTTTCTT
TTGGGTGCTT   5460

GAGTTTCATT AGGCTGAGCT GACTCGTTGC TCTCTAGTCT TTCATCTCTG
TCTTTTCCAA   5520

GGATTCATAA CGTTGGTCGC TCTCTGTTTC TGCCTACACT TCTTCAAGGG
ATCATTACTG   5580

AGGCTAAGAG TTAAAGACCT GAACCATGGT TTTCTGTAAC TGGTTCAAGT
TCATTCTCCG   5640

GTTATTGTGT GGTTATCTTT CGGTTAGATT GAAACCCATA TGTTTGCTCT
GTTTCTTCTA   5700

GTTCCAAGTT TAATTTCCGG TTATTGTTTG GCTTTTTAAA AGTTTTTAAG
GTCTATTCTA   5760

TGTAAAGACT ATTCTACGTA CGTACATTTA TCGCAAAATT GAAAGATTAT
AAAAAAAATT   5820

GAAAGATCCA AAGGAAACCA ATAGATTAAA CTAAAATGTA GTATCCTTTT
TATCATTTTA   5880

GGCTATGTTT TCTTTTAAGA AAGCTTTGGT AGTTAACTCT GTTTAAAAGA
AAAAAAAGAG   5940

ATGCATAAAT TAAATTTAAG TTTCTAGAAC TTTTGGATAA ACATATTAAG
CTAAAGAAAT   6000

TAAACTAAAG GGCGTAAATG CAAGCTTGTT ATGCGTTATT GAAAACATTA
CCTCTAAATT   6060

AAATAGCCCA ATATTGAAAA CCTTAAGCTT CTTTGATCCC CTTAACTTGT
TTGTCCACCA   6120

AGTATTAGTT CATCTCTTAA CACGGCAACT CGAAACGGCA CAATGGACAA
ACATGGTCTT   6180

TCAAAAACCA CTTCCCAATA CATCCATCGT CAAACTCGTG GCCACATGGT
AAGGTCACCA   6240

CTATTTCTCC CTTTTCAAAC TCCTCCAAAC AAATTGTGCA CACACTGGCG
TCAGAGTTGG   6300

ATTTCTTCTT ATTATTATAT ACTTTCCTTG CCAAACGGTC AACCACAAAC
TTATTTGCCG   6360

GTCTAATTAA CTCGATATTA TTGGTGGTCT CATCAAACGA GTCAATCCGA
GGAGGAGGTG   6420

GAACAATGAC TTTACAGTAC ATGTAAACTA ACGTAGCACA AACTGAAGAG
TCTACCATAG   6480

AAATCGACTT ACAGATTCGT TCAGTGAGTT GAGAGTTAGC AATGTCAACA
TATTGTTCGG   6540

AGAGCCCTGC TGAGTACAAC CATTCATTCA GTTTTTTCGA GTCATTAGGG
TAGGAGGATA   6600

TGACACCTTC GTAGTCATTG TACGAGAGAA CGAAATTTGG TGGAAGACTA
ATTGATGTGT   6660

CCGATCTTCG GGCACTTACG CAGATTTTGA ATGATCCAGC ATCTTGTGAT
TTCGGTTTGA   6720

GGTCTATTTC GCCGCCAAAG GATATTTCCG CTTCCATAGC TATCAAAGAG
AAAGAAAAAT   6780

AGTGAATCCA AGGTTTAGGG TTTCTTTTCT TTGTCTTNCT TATATATAGA
GGCGCTAGAT   6840

TGTATTAAGG ATTATACATA TATATAAGTA ATTGCAATTT GTGAGTTTAT CCTTATTCAT   6900

TTTTAATTTT ATTTACCTTT ATTTAGTTGA TATTGTGTCC TTTTCCTAGG TAGCATTTCC   6960

TTCCATCTGT GTTAATTATT AGCATTTCCT TTCCTTTGTC TTATTTGCCT TTATTTCGTA   7020

GGAAGAAATC CTTTATGNAC CCCATCTTGG CTGAGAACTT GAGATGATTT TAAATCCTCA   7080

AAAATTATTC AATTTATGAT TTCGAAATTG ATATACACTT TATATTTTCT CCTAAAAAAC   7140

CATATTGTAC TAAGAAAAGT AGAAAACCAG ACTTTTTAAT ATGTTAGATT TTAATTGGGT   7200

TCTTAAAGTG TTTTAGCGTT TNACACCGGT TATTCTCCAA AATCCAAACT CTATAATTAT   7260

AGTTTTTAAG TATAAATTAA TCCGGTTGGC CCAATTAGTG GACCGTTTAA AGAGTAGACA   7320

CTTTTTTTTT TATATATCGA CTACCATAAA ACTTTAACGA TTAATATTTT TGGATAATAA   7380

GCGATCGTTT TGAGGCGTCC CAATTTTTTT TGTTTCTTTT TATATGAGAA ATGGGTTTAA   7440

GAAAAACTGC AATTTTGTCC ATAAAGCTAG TCAGAATTCC TGCAGCCCGG GGGATCCACT   7500

AGTTCTAGAG CGGCCGCCAC CGCGGTGGAG CTCCAATTCG CCCTATAGTG AGTCGTATTA   7560

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 7 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Pro Ile Ala Asn Val Ile
1   5

(2) INFORMATION FOR SEQ ID NO:6:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 12 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val
1   5   10

(2) INFORMATION FOR SEQ ID NO:7:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCAGC AACAACCCAA CCCCA   25

(2) INFORMATION FOR SEQ ID NO:8:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 27 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCTAGACA TACAACACTT TTCCTTA   27

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACCAGCT CAGTCATAGT AGC   23

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCACACATG GTGGTTGCTG CTG   23

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGATAGAGA CCGATCGTGG TTC   23

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 24 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCACTTATAC TGACCATAAT GGTC   24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 24 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCATAGATGC ACTCGAAATC AGCC   24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 22 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTTGGTAAT AATTGTCATT AG   22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTAAAAACAT CTACGGTTCA   20

(2) INFORMATION FOR SEQ ID NO:16:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTGTGGTTG ACCGTTTGGC   20

(2) INFORMATION FOR SEQ ID NO:17:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 7 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Pro Ile Ala Asn Val Ala
1   5

(2) INFORMATION FOR SEQ ID NO:18:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 12 amino acids
    (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val
1   5   10

SEQ ID NO:19: *Arabidopsis* L1L gene (pMNJ7 sequence)

```
ATGGCAGAGG GCAGTATGCG TCCTCCAGAA TTCAACCAGC CTAACAAAAC
CAGTAATGGT GGTGAGGAGG AGTGCACGGT GAGGGAGCAA GACAGGTTCA
TGCCTATTGC CAACGTGATA CGGATCATGC GGAGGATCTT ACCTGCTCAC
GCCAAGATCT CAGATGACTC CAAGGAGACG ATCCAAGAGT GTGTTTCGGA
GTACATCAGC TTCATAACAG GGGAGGCTAA TGAGCGGTGC CAGCGGGAAC
AGCGCAAGAC CATCACTGCT GAGGACGTCT TGTGGGCAAT GAGCAAGCTC
GGTTTTGATG ACTACATCGA ACCCCTCACG TTGTACCTCC ACCGCTACAG
AGAGTTGGAA GGTGAAAGAG GGGTTAGCTG CAGTGCTGGG TCCGTTAGTA
TGACCAACGG CTTGGTGGTC AAGAGGCCTA ATGGGACCAT GACCGAGTAT
GGAGCCTACG GCCTGTGCC AGGGATTCAC ATGGCGCAGT ACCATTATCG
TCATCAGAAC GGGTTTGTTT TCAGTGGTAA CGAACCTAAT TCTAAGATGA
GTGGTTCATC TTCAGGAGCA AGTGGCGCCA GAGTTGAAGT ATTTCCGACT
CAACAACATA AGTACTGA
```

SEQ ID NO:20: *Arabidopsis* L1L protein

```
MAEGSMRPPE FNQPNKTSNG GEEECTVREQ DRFMPIANVI RIMRRILPAH
AKISDDSKET IQECVSEYIS FITGEANERC QREQRKTITA EDVLWAMSKL
GFDDYIEPLT LYLHRYRELE GERGVSCSAG SVSMTNGLVV KRPNGTMTEY
GAYGPVEGIH MAQYHYRHQN GFVFSGNEPN SKMSGSSSGA SGARVEVFPT
QQHKY
```

SEQ ID NO:21: *Phaseolus* gene

```
GATCTCTCAACCCAACCCTTTCATTTTCATTTTCATTTTCATTTTTCCATCACTTCACTGTC
ACCATGGAAAG
TGGAGGCTTTCATGGCTACCGCAAGCTCCCAACACCACCTCTCCTGGGTTGAAGCTGTCAG
TGTCAGACATG
AACAACGTGAACACGAGTAGGCAGGTAGCAGGAGACAACAACCATACAGCGGATGAGAGCAA
CGAATGCACTG
TGAGGGAGCAAGACCGTTTCATGCCAATTGCAAATGTGATCAGGATCATGCGAAAGATTCTT
CCTCCACATGC
CAAGATCTCAGGTGATGCCAAAGAAACAATTCAAGAGTGTGTGTCTGAGTACATCAGCTTTA
TCACCGGAGAG
GCAAACGAGCGTTGCCAGAGGGAACAACGCAAGACCATAACTGCTGAGGACGTGCTTTGGGC
CATGAGCAAGC
```

TTGGATTTGATGATTACATGGAGCCACTGACCATGTACCTTCACAGGTATCGTGAGCTTGAG
GGTGACCGAAC
CTCCATGAGAGGTGAATCATTGGGGAAGACGACTATTGAATACGCCCCTATGGGTGTTGGCG
TTGCTACTGCT
TTTGTGCCACCACAGTTTCACCCAAATGGATACTATGGTCCTGCCATGGGAGCTTACGTTGC
GCCACCAAATG
CTGCGTCCTCTCATCACCATGGAATGCCAAATACTGAACCGAATGCTCGCTCCATGTGAATT
GATGATGATGA
GGAGGAGGAGGAGGAAGACGACGAGTGTTGAGTTAGTAGAAGAAGAATACTTTAATTAATTA
GCTTAACTCTC
GGTAATTAGAGTACTGTTGTTGAGGGTACGTAGTAAACTTTATAATTAAGGGGATGGATGGG
ATTAAGGAGTT
CTGATATTCCTAATCCTAATCAGGCCTATGTTAATTTATGTAATAACTCTGCTTATGTTTTT
GGATTTTCTGA
TGTTGTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:22: *Phaseolus* protein

MESGGFHGYPKLFNTTSPGLHLSVSDMNNVIITSPQVAGDHHHTADESHECTVPEQDRFMPIA
NVIFIMRKILP
PHAKISGDAKETIQECVSEYISFITGEANEPCQREQFKTITAEDVLWAMSKLGFDDYMEPLT
MYLHPTPELEG
DPTSMEGESLGERTIEYAPMGVGVATAFVPPQFHPNGYYGPAMGAYVAPPHAASSHHHGMPN
TEPHARSM

SEQ ID NO:23: 5' untranslated region

```
gatatggaac gtggaggctt ccatggctac cgcaagctgt ccgtgaacaa caccactcct
tctccaccag gtagtgccat tctctatacc ccctcttttc acaggctctc ttcatttcag
ttgcatgcga aaccattctc tgcaatccct ccattgtcat gtctgtactc tttrcatgac
gaacagttaa tgaaatagct tttcaatctt ataaaccgcg catgcagacg tcatccgaagc
cattatgcac taaaacttcc attttctta tttttgttag gattagcagc gaattttctg
```

SEQ ID NO:24: 3' untranslated region

```
                      aa acaatggcta ataacataga cagctgacag agtcataact
gttagtaggt gcaagctgta gcttatgaat tcaagtttaa gcgaaaacaa tgctgcttt
tctttgttta ttatctatct agttgaaaga acattgtgtt tttcatctga tctgtcttgt
ggtaaagtat gtcaataaag cattagtttt gcaaaccuca tgcatgtgat attacaaaat
tcacggtgaa ttcgtaatgc gtcttggttc aaaatagaaa gagactaaac attccagatt
tcaattctca gctacagaaa tgagtgutta acggatacag aaacaactct cacaatcttc
attcatttca tttagctact actttcaaa ggaacttcaa cgcatacctt tttcctctcc
agaagatcat gtttgtctgc actctcgttt gcctcagtat cttctcctg atgctcttca
gatatatgtt ccaatttcga acaatcaaca ggatcaagtc cggttctttt cctctgagga
atcacagtga agaaggctgt tttccagtcc ctagtctcca gaaacttgac gagtatctcc
aaaacttggt tcacagtgag aacctaaatc aataaaaacc acaaatctta cattaacaaa
gtacataaag tagaggtttt ttgtgttgtg cccaatgaga caagaattga agtggccatt
tagttacctg agaacttgac attttcatat actctcctat gggaagctta gctgtttaa
tgccttgttc ttgagccttg gtcatggtga tccctttgaa ccggtttcga tccactaagc
caccgataat gtagatatgc ttagggtcaa gatcatccaa aacagtttca gaatcagccg
taagatacac caaattatct ttctgatcag ccatggcttc aatgtaacac ctactttcct
tttcaatgaa ccatttctca aaaccaggaa gcttgtcaag ctcagtactc atcttccc
```